

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ni, Jian
Rosen, Craig A.
Gentz, Reiner L.
Lyn, Sally Doreen Patricia
Hurle, Mark Robert
- (ii) TITLE OF INVENTION: Human Tumor Necrosis Factor
Receptor-Like 2
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
(B) STREET: 1100 New York Ave, Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/464,595
(B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/462,962
(B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/462,315
(B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US95/05058
(B) FILING DATE: 27-APR-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.0770004/EKS/SGW
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-271-2600
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1704 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 265..1113

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 265..372

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 373..1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGCTG CCTCCCGCAG GCGCCACCTG TGTCCCCCAG CGCCGCTCCA CCCAGCAGGC	60
CTGAGCCCCT CTCTGCTGCC AGACACCCCC TGCTGCCCAC TCTCCTGCTG CTCGGGTTCT	120
GAGGCACAGC TTGTCACACC GAGGCGGATT CTCTTTCTCT TTCTCTTTCT CTTCTGGCCC	180
ACAGCCGCAG CAATGGCGCT GAGTTCCTCT GCTGGAGTTC ATCCTGCTAG CTGGGTTCCC	240
GAGCTGCCGG TCTGAGCCTG AGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT	291
Met Glu Pro Pro Gly Asp Trp Gly Pro	
-36 -35 -30	
CCT CCC TGG AGA TCC ACC CCC AAA ACC GAC GTC TTG AGG CTG GTG CTG	339
Pro Pro Trp Arg Ser Thr Pro Lys Thr Asp Val Leu Arg Leu Val Leu	
-25 -20 -15	
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC	387
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
-10 -5 1 5	
TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC	435
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
10 15 20	
AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA	483
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
25 30 35	
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC	531
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
40 45 50	

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ACACCCAGCC CTCCTGGGCC AACCCAGAGG GCCTTCAGAC CCCAGCTGTG TGC GCGTCTG 1463
 ACTCTTGTGG CCTCAGCAGG ACAGGCCCCG GGCCTGCCT CACAGCCAAG GCTGGACTGG 1523
 GTTGGCTGCA GTGTGGTGT TAGTGGATAC CACATCGGAA GTGATTTTCT AAATTGGATT 1583
 TGAATTCGGC TCCTGTTTTT TATTTGTCAT GAAACAGTGT ATTTGGGGAG ATGCTGTGGG 1643
 AGGATGTAAA TATCTTGT TT CTCCTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1703
 A 1704

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 -36 -35 -30 -25
 Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10 -5
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 1 5 10
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 30 35 40
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 45 50 55 60
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 65 70 75
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 80 85 90
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 95 100 105
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 110 115 120
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
 125 130 135 140
 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
 145 150 155

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Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
 160 165 170
 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
 175 180 185
 Val Lys-Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
 190 195 200
 Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
 205 210 215 220
 Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
 225 230 235
 Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
 240 245

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15
 Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
 20 25 30
 His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
 35 40 45
 Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60
 Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80
 Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95
 Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110
 Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125
 Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140

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Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
180 185 190

Arg Ala Leu Leu Val Ile Pro Val Val Met Gly Ile Leu Ile Thr Ile
195 200 205

Phe Gly Val Phe Leu Tyr Ile Lys Lys Val Val Lys Lys Pro Lys Asp
210 215 220

Asn Glu Met Leu Pro Pro Ala Ala Arg Arg Gln Asp Pro Gln Glu Met
225 230 235 240

Glu Asp Tyr Pro Gly His Asn Thr Ala Ala Pro Val Gln Glu Thr Leu
245 250 255

His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile
260 265 270

Ser Val Gln Glu Arg Gln Val Thr Asp
275 280

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 373..927

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 373..480

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 481..927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCCCTTCTA CAGGAAACCC GGAGTGGACT GGAACGGTGC AGGGGGAGAA CTCGCCCCCTC 60

CCATCGGGCG CCTCCTTCAT ACCGGCCCTT CCCCTCGGCT TTGCCTGGAC AGCTCCTGCC 120

TCAGGCAGCG CCACCTGTGT CGCCCAGCGC CGCTCCACCC AGCAGGCCTG AGCCCCCTCTC 180

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TGCTGCCAGA CACCCCCTGC TGCCCACTAC TCCTGCTGCT CGGGTTCTGA GGCACAGCTT	240
GTCACACCGA GCGGATTCT CTTTCTCTTT CTCTTTCTCT TCTGGCCAC AGCCGCAGCA	300
ATGGCGCTGA GTTCCTCTGC TGGAGTTCAT CCTGCTAGCT GGGTTCCCGA GCTGCCGGTC	360
TGAGCCTGAG TC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG	408
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp	
-36 -35 -30 -25	
AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC	456
Arg Ser Thr Pro Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr	
-20 -15 -10	
TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG	504
Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu	
-5 1 5	
GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT	552
Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly	
10 15 20	
TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA	600
Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu	
25 30 35 40	
CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG	648
Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys	
45 50 55	
TGT CTG CAG TGC CAA ATG TGT GAC CCA GAT ATT GGT TCC CCC TGT GAC	696
Cys Leu Gln Cys Gln Met Cys Asp Pro Asp Ile Gly Ser Pro Cys Asp	
60 65 70	
CTC AGG GGA AGA GGT CAC CTG GAG GCT GGT GCC CAC CTG AGT CCA GGC	744
Leu Arg Gly Arg Gly His Leu Glu Ala Gly Ala His Leu Ser Pro Gly	
75 80 85	
AGA CAG AAA GGG GAA CCA GAC CCA GAG GTG GCC TTT GAG TCA CTG AGC	792
Arg Gln Lys Gly Glu Pro Asp Pro Glu Val Ala Phe Glu Ser Leu Ser	
90 95 100	
GCA GAG CCT GTC CAT GCG GCC AAC GGC TCT GTC CCC TTG GAG CCT CAT	840
Ala Glu Pro Val His Ala Ala Asn Gly Ser Val Pro Leu Glu Pro His	
105 110 115 120	
GCC AGG CTC AGC ATG GCC AGT GCT CCC TGC GGC CAG GCA GGA CTG CAC	888
Ala Arg Leu Ser Met Ala Ser Ala Pro Cys Gly Gln Ala Gly Leu His	
125 130 135	
CTG CGG GAC AGG GCT GAC GGC ACA CCT GGG GGC AGG GCC TGAGCCTACA	937
Leu Arg Asp Arg Ala Asp Gly Thr Pro Gly Gly Arg Ala	
140 145	
GGGAGGCACA GGGCAGGTGG GCTAGCCATG AACAGAAGAG GAAGCTGGAG TGCTTTGGGG	997
GTTTCATGCAT GTAGGCTGGG ATTTGGGGCT CACACCTCAA CCTGCATGCC CAGTTCCATG	1057
CCCCTCCCCT CTTGTGAAAG CACCTGTCTA CTTGGGCTGA GGATGTGGGG GCACAGGTGG	1117

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CAGGTGAGGC TGCCCTCAGG AGGGGCCCAG GCCCAGCTTG TACCCACCT CCACCAGTAC	1177
CTGAAGAAGT GGGGCTCTCA CCCTACCTGC CTCTGCCATT GGAATGGCCT GGTTTGCACA	1237
GATGGGAAAC CCGTTTGAGG GGTGGGTGTC TGGGTGGGCA CGTGGGGCGA GGACCTGCCT	1297
GAGGGACCCT GCCCTGGAAC TGACAGTGCA AGCTEGGCGT CCTGCCCATC TGGGCAGAAG	1357
GCTGGTTTCT CCCATCAACG AAGCCCTCCC AGGACCTTCC TGCAAGCCCT CGTCCCACAC	1417
GCAGCTCTGC CGTCCCTTGG TGTCCCTCCC GGCCTCAGGT CCTCCATGCT GGGTACCTCT	1477
GGGCACCTCG TTTGGCTGAG CCAGGGGTTC AGCCTGGCAG GGCGCCCTGG CAGCAGTCCT	1537
TGGCCTGTGG ATGCTGTCCT GGCTGTGGA TGGTGTCCCG CCCTCCACGT ACCCCTCTCA	1597
CCCCCTCCTC TTGGACTCCA GCCATGGGCC TGC GCGCAG CCGGAACTGC TCCAGGACAG	1657
AGAACGCCGT GTGTGGCTGC AGCCCAGGCC ACTTCTGCAT CGTCCAGGAC GGGGACCACT	1717
GCGCCGCGTG CCGCGCTTAC GCCACCTCCA GCCCGGGCCA GAGGGTGCAG AAGGGAGGCA	1777
CCGAGAGTCA GGACACCCTG TGT CAGA ACT GCGCGCGG GACCTTCTCT CCAATGGGA	1837
CCCTGGAGGA ATGTCAGCAC CAGACCAATT GGCCTAATCA TATGTGTGAA AAGAAGAAAG	1897
CCAAGGGGTG AGCACACGGT GGCCCCATCA GGGTTCATGT CCCCAGCCGT CACCTCTTGG	1957
AGCTCTGTCA CCCCAGCCT GGGAGGTGGC CCCAGAGCTT TTCCAGGATC CGCGGCTCCT	2017
CCCAGGGCAG CCACTGCAGG CTGGGGCAGG TGTATGTAGT CAAGGTGATC GTCTCCGTCC	2077
AGCGGTAAAA GACAGGAGGC AGAAGGTGAG GCCACAGTCA TTGAGCCCTG CAGGCCCCCTC	2137
CGGACGTCAC CACGGTGGCC GTGGAGGAGA CAATACCCTC ATTCACGGGG AGGAGCCCAA	2197
ACCACTGACC CACAGACTCT GCACCCCGAC GCCAGAGATA CCTGGAGAGA CGGCTGCTGA	2257
TAGAGGCTGT CCACCTGGCG AAACCACCGG AGCCCGGAGG CTTGGGGGCT CCGCCCTGGG	2317
CTGGTTTCCG TCTCCTCCAG TGGAGGGAGA GGTGGTGCCC CTGCTGGTGG TAGAGCTGGG	2377
GACGCCACGT GCCATTCCCA TGGTTCAGTG AGGGGCTGGT GGCCTCTGTT CTGCTGTGGC	2437
CTGAGCTCCC CAGAGTCCTG AGGAGGAGCC CCAGTTGCCC CTCGCTCACA GACCACACAC	2497
CCAGCCCTCC TGGGCCAACC CAGAGGCCCC TTCAGACCCC AGCTGTCTGC GCGTCTGACT	2557
CTTGTTGGCCT CAGCAGGACA GGCCCCGGGC ACTGCCTCAC AGCCAAGGCT GGAATGGGTT	2617
GGCTGCAGTG TGGTGTTTAG TGGATACCAC ATCGGAAGTG ATTTTCTAAA AATTGGATT	2677
GAATTCGGAA AAAAA	2692

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

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Cmt

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-36 -35 -30 -25
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10 -5
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55 60
Gln Met Cys Asp Pro Asp Ile Gly Ser Pro Cys Asp Leu Arg Gly Arg
65 70 75
Gly His Leu Glu Ala Gly Ala His Leu Ser Pro Gly Arg Gln Lys Gly
80 85 90
Glu Pro Asp Pro Glu Val Ala Phe Glu Ser Leu Ser Ala Glu Pro Val
95 100 105
His Ala Ala Asn Gly Ser Val Pro Leu Glu Pro His Ala Arg Leu Ser
110 115 120
Met Ala Ser Ala Pro Cys Gly Gln Ala Gly Leu His Leu Arg Asp Arg
125 130 135 140
Ala Asp Gly Thr Pro Gly Gly Arg Ala
145

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2637 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 247..654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGCTCGGG CTCCACCGGG GACGACCGCT CCTAGAAACT GAGTGGTATC CCCCAGGCGCT	60
GCAGGAATTC CAACCTGCCT GAAGGGACCC TGCCCTGGAA CTGACAGTGC AAGCTCGGCG	120
TCCTGCCCAT CTGGGAAGAA GGCTGGTTTC TCCCATCAAC GAAGCCCTCC CAGGACCTTC	180
CTGCAAGCCC TCGTCCCACA CGCAGCTCTG CCGTCCCTTG GTGTCCCTCC CGGCCTCAGG	240
TCCTCC ATG CTG GGT ACC TCT GGG CAC CTC GTT TGG CTG AGC CAG GGG	288
Met Leu Gly Thr Ser Gly His Leu Val Trp Leu Ser Gln Gly	
150 155 160	
TTC AGC CTG GCA GGG CGC CCT GGC AGC AGT CCT TGG CCT GTG GAT GCT	336
Phe Ser Leu Ala Gly Arg Pro Gly Ser Ser Pro Trp Pro Val Asp Ala	
165 170 175	
GTC CTG GCC TGT GGA TGG TGT CCC GGC CTC CAC GTA CCC CCT CTC AGC	384
Val Leu Ala Cys Gly Trp Cys Pro Gly Leu His Val Pro Pro Leu Ser	
180 185 190 195	
CCC TCC TCT TGG ACT CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC	432
Pro Ser Ser Trp Thr Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys	
200 205 210	
TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC	480
Ser Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys	
215 220 225	
ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC	528
Ile Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr	
230 235 240	
TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC	576
Ser Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp	
245 250 255	
ACC CTG TGT CAG AAC TGC CCC CGG GGA CCT TCT CTC CCA ATG GGA CCC	624
Thr Leu Cys Gln Asn Cys Pro Arg Gly Pro Ser Leu Pro Met Gly Pro	
260 265 270 275	
TGG AGG AAT GTC AGC ACC AGA CCA AGT AAG TGAACCCGGG GGAGGCCAGC	674
Trp Arg Asn Val Ser Thr Arg Pro Ser Lys	
280 285	
TCTGTGCCCT GGGGAGGGGG CTCCACGTTG CTTCCCTGGG AGATGACCGT CTTCTCCAGC	734
AGAAAGGTTG AAGGTCCCAC CCTGAGCGGC ACCCTGGTCA CATGCCTGCG TCCAGGAGAG	794
CTGCAGGGTG AAGCCTGTGT GCCCCAGATA ACCCCTTCCA TGGGCCCAGA CAAAGCCTCA	854
TCAGATCTGA GCTTCCTGGA GGCTCAGGAT GGGCCTTCCC AGAAGCAGGC CCAGAGGGAG	914
GCTGCCTCCA GATCCCCTGT CCCCTGGGGC TGTGGGTGTC CCTGAATGTC AGGGCCATGG	974

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GAGGGCCCCT GGGCTTCAGG GGTGTTGGGAA AGTGAACACT CTGCTCTTTG TCCACCTTCG 1034
GGAGGACAAC CTTCAAATGC TGACCCTGGG CCCCTAACTG ACCTGAGACT TCAGAGCTTC 1094
TTGGGAGGAG CTGGGGTCCC CCAGCGGAGC CTGGGATGGA GCAGGGATGG CTGCCCCAGG 1154
GAGGGGGCGG TGGGGCCTTC CATCCTGCTC TGCCCTCCTC GTCCTCTGGC CCCAGCTCAG 1214
TCCTGTCCAT CTCCAGCTCT AACCATTGTG GGCCCGACAC TGGCTCTCCC TCTACCTTCT 1274
GTCCTTGTCT GAACTGGTC TCCCGTGCTC TGGGGTCTCT GAACTGATGG CTGCCTCCCG 1334
CTTCTCTCCC CTCTCCCTCT GCCGTCTGT CTCTGTGGC CAGTCTCTCC TTGTTTCTCT 1394
TCTCCTCCTT CTTTCTCTCC ACCTCCCCAT AGCCGAGCTT GGAAAAGTCA GACAGACCTC 1454
TGAGGTCTCA TCCTGGAGCT GCCACCAGCC CAGCCTCCCT GGGACCTGTC TTCCTGCCT 1514
GGGGCCCTGG GAGCCAGGGA GGCTCCCTGA GGCTGAGTGA AACTGGGCG CTGCACCTGC 1574
CTCTCCCACG TCCTCGGCCC CACTCCCGCA GGTGCAGCTG GCTGGTGACG AAGCCCGGAG 1634
CTGGGACCAG CAGCTCCAC TGGGTATGGT GGTTCCTCTC AGGGAGCCTC GTCATCGTCA 1694
TTGTTTGCTC CACAGTTGGC CTAATCATAT GTGTGAAAAG AAGAAAGCCA AGGGGTGATG 1754
TAGTCAAGGT GATCGTCTCC GTCCAGGTAT TGATCCTCCT CCCCTCTCC CTCCCCCTC 1814
CACCTTCCCA CCTCCCTCT CCCCGCTGGG GCTGGTGTTT CTGGTGTACA TGGTGGGGGC 1874
TCCCAGTTCT CTGAGGGTCC TGAGTCTTTC AAGTACAGCC ACGGTAGCTC AGGAAAGAAC 1934
CCACCCCTC AAAGTAAAG CAGTAAATG AACCCGAGAA CCTGGAGTCC CAGGGGGGCC 1994
TGAGCAGGCA GGGTCTCCAC GATTCGTGTG CTCACAGCGG GAAAAGACAG GAGGCAGAAG 2054
GTGAGGCCAC AGTCATTGAG GCCCTGCAGG CCCCTCCGGA CGTCACCACG GTGGCCGTGG 2114
AGGAGACAAT ACCCTCATTC ACGGGGGAGG AGCCCAAACC ACTGACCCAC AGACTCTGCA 2174
CCCCGACGCC AGAGATACCT GGAGCGACGG CTGCTGAAAG AGGCTGTCCA CCTGGCGAAA 2234
CCACCGGAGC CCGGAGGTTT GGGGGCTCCG CCCTGGGCTG GTTCCGTCT CCTCCAGTGG 2294
AGGGAGAGGT GGGGCCCCTG CTGGGGTAGA GCTGGGGACG CCACGTGCCA TCCCATGGG 2354
CCAGTGAGGG CCTGGGGCCT CTGTTCTGCT GTGGCCTGAG CTCCCAGAG TCCTGAGGAG 2414
GAGCGCCAGT TGCCCTCGC TCACAGACCA CACACCAGC CCTCCTGGGT CCAGCCCAGA 2474
GGGCCCTTCA GACCCAGCT GTCTGCGCGT CTGACTCTTG TGGCCTCAGC AGGACAGGCC 2534
CCGGGCACTG CCTTCAAGCC AAGGCTGGAC TGGGTTGGCT GCAGTGTGGT GTTTAGTGGA 2594
TACCACATCG GAAGTGATTT TCTAAATTGG ATTTGAAAAA AAA 2637

(2) INFORMATION FOR SEQ ID NO:8:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Leu Gly Thr Ser Gly His Leu Val Trp Leu Ser Gln Gly Phe Ser
 1 5 10 15
 Leu Ala Gly Arg Pro Gly Ser Ser Pro Trp Pro Val Asp Ala Val Leu
 20 25 30
 Ala Cys Gly Trp Cys Pro Gly Leu His Val Pro Pro Leu Ser Pro Ser
 35 40 45
 Ser Trp Thr Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg
 50 55 60
 Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val
 65 70 75 80
 Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser
 85 90 95
 Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu
 100 105 110
 Cys Gln Asn Cys Pro Arg Gly Pro Ser Leu Pro Met Gly Pro Trp Arg
 115 120 125
 Asn Val Ser Thr Arg Pro Ser Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45

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Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser-Thr Tyr Thr-Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala
 195

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
 1 5 10 15
 Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly
 20 25 30
 Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
 35 40 45
 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
 50 55 60
 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
 65 70 75 80

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 cont.

Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
85 90 95
Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
100 105 110
His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
115 120 125
Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
130 135 140
Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu
145 150

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10 15
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
20 25 30
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
35 40 45
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
50 55 60
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
65 70 75 80
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
85 90 95
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
100 105 110
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
115 120 125
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
130 135 140
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
145 150 155 160

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Cont.

Val Cys Thr

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu	Ile	Asn	Ser	Gln	Cys	Cys	Ser	Leu
1				5					10					15	
Cys	Gln	Pro	Gly	Gln	Lys	Leu	Val	Ser	Asp	Cys	Thr	Glu	Pro	Thr	Glu
			20					25					30		
Thr	Glu	Cys	Leu	Pro	Cys	Gly	Glu	Ser	Glu	Phe	Leu	Asp	Thr	Trp	Asn
		35				40						45			
Arg	Glu	Thr	His	Cys	His	Gln	His	Lys	Tyr	Cys	Asp	Pro	Asn	Leu	Gly
	50					55					60				
Leu	Arg	Val	Gln	Gln	Lys	Gly	Thr	Ser	Glu	Thr	Asp	Thr	Ile	Cys	Thr
65					70					75					80
Cys	Glu	Glu	Gly	Trp	His	Cys	Thr	Ser	Glu	Ala	Cys	Glu	Ser	Cys	Val
				85					90					95	
Leu	His	Arg	Ser	Cys	Ser	Pro	Gly	Phe	Gly	Val	Lys	Gln	Ile	Ala	Thr
			100					105					110		
Gly	Val	Ser	Asp	Thr	Ile	Cys	Glu	Pro	Cys	Pro	Val	Gly	Phe	Phe	Ser
		115					120					125			
Asn	Val	Ser	Ser	Ala	Phe	Glu	Lys	Cys	His	Pro	Trp	Thr	Ser	Cys	Glu
	130					135					140				
Thr	Lys	Asp	Leu	Val	Val	Gln	Gln	Ala	Gly	Thr	Asn	Lys	Thr	Asp	Val
145					150					155					160
Val	Cys	Gly													

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

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Cont.

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln
 1 5 10 15
 Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln
 20 25 30
 Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg
 35 40 45
 Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly
 50 55 60
 Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys
 65 70 75 80
 Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly
 85 90 95
 Thr Phe Asn Lys Gln Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys
 100 105 110
 Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp
 115 120 125
 Val Val Cys Gly
 130

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCCCATGGC CCCAGCTCTG CCGTCCT

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCAAGCTTA TTGTGGGAGC TGCTGGTCCC

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGATCCC GGAGCCCCCT GCTAC

25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGTACCA TTGTGGGAGC TGCTGGTCCC

30

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCGCGGATCC ACCATGGAGC CTCCTGGAGA CTGG

34

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGCGGTACC TCTACCCCGAG CAGGGGCGCC A

31

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGCGGATCC ACCATGGAGC CTCCTGGAGA CTGG

34

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCGCTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA GTGGTTTGGG CTCCTCCC

58

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCGCGGATCC ACCATGGAGC CTCCTGGAGA CTGG

34

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAATTCG CAGCCATGGA GCCTCCTGGA GACTG

35

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATACCCAG GTACCCCTTC CCTCGATAGA TCTTGCCTTC GTCACCAGCC AGC

53

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